

(1) GENERAL INFORMATION:

(i) APPLICANT: Greenspan, Daniel S
Takahara, Kazuhiko
Hoffman, Guy G

10 (ii) TITLE OF INVENTION: Mammalian Tolloid-Like Protein

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Quarles & Brady
(B) STREET: 1 South Pinckney Street
(C) CITY: Madison
(D) STATE: WI
(E) COUNTRY: US
(F) ZIP: 53703

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0,
Version #1.30

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

30 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Berson, Bennett J
(B) REGISTRATION NUMBER: 37094
(C) REFERENCE/DOCKET NUMBER: 960296.93839

35 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 608-251-5000
(B) TELEFAX: 608-251-9166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide probe"

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGTCCAGAC CGGAGCGGGT GTGGCCCGAT GGGTCATCC CGTTTGTGAT TGGAGGGAAAT 60

TTCACAGGCA GCCAGAGGGC AGTCTTCCGG CAGGCCATGA GACACTGGGA GAAGCATACC 120

TGTGTCACCT TCTTGGAGCG CACAGATGAG GACAGCTATA TTGTATTACAC CTACCGACCC 180

TGCGGGTGCT GCTCCTACGT GGGTCGCCGA GGTGGGGGCC CCCAGGCCAT CTCCATCGGC 240

50 AAGAACTGTG ACAAGTTGG CATCGTGGTC CATGAGCTGG GCCATGTCAT TGGCTTCTGG 300

CACGAGCACA CGCGGCCCGA CCGCGACCGC

330

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

10

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 611..3652
- (D) OTHER INFORMATION: /product= "murine mT11 protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACACCCCTT TGCTCTCCGG GCAGTCGGGA GCTTCCCTAG CTTCCGCAGG CTTTTAAGGT 60
CTGGCGGCGT AGAAATGCCT ATCCCCCACC CCCTTCCTCG GTCTCCCCTT TCAGTTCAGA 120
TGTGCTGATG TGCAGACCGG ATTCACTCTTC CCCGAGCAGC GGCGGTGGCA GCGGCGGGCG 180
CAGGCAGGCTG CAGCTCGCTC TCGGCCGCGG GGTCTGACA GCGGCGGGGG CGCGGCGCGG 240
GAGCCGGAGC TCCGGTGGCA GCTGAGCCCG CCGTGCGCCT CTCGCCGCGG CCGGTCGTGA 300
TCGCGGGAAAG TTGAGCCGCT GGAAGGACGA CCTAGACCGA GCGGGGTTGG CTGCGGCTGC 360
CCTGCGCCGA GCTCCTCACC TGCCTTCGCG CCACCCGCGG GCCCCCGGCC AAGTTCCCCA 420
GCATCCGGGG GAGACAGGGG GACATTGCCC CTCTCTAGCG TCCTGAAGAC ATCCGCATGT 480
CTCCGGACAC CTGAACATTC AGGTCTTTCC GAGGAGCTTC CCAGTCGGGA TAAGAACACT 540
GTCCCTAGAG CCCCGCATAT CCACGCGGCC CTCCGGGTCT GGTCCCTCTC TTTCCCTCTA 600
GGGGAGGAGG ATG GGT TTG CAA GCG CTC TCC CCG AGG ATG CTC CTG TGG 649
Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp
25 1 5 10

TTG GTG GTC TCG GGT ATT GTT TTC TCC CCG GTG CTG TGG GTC TGC GCT 697
Leu Val Val Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala
15 20 25

30 GGC CTC GAT TAT GAT TAC ACT TTT GAT GGG AAC GAA GAG GAC AAA ACG 745
Gly Leu Asp Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr
30 35 40 45

GAG CCT ATA GAT TAC AAG GAC CCG TGC AAA GCT GCT GTG TTT TGG GGT 793
Glu Pro Ile Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly
50 55 60

35 GAC ATC GCC TTA GAT GAT GAA GAC TTA AAT ATC TTC CAA ATA GAC AGG 841
Asp Ile Ala Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg
65 70 75

40 ACA ATT GAC CTG ACC CAG AGC CCC TTT GGA AAA CTT GGA CAT ATT ACA 889
Thr Ile Asp Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr
80 85 90

GGT GGC TTT GGA GAC CAT GGC ATG CCA AAG AAG CGA GGG GCA CTC TAC 937
Gly Gly Phe Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr
95 100 105

	CAA CTT ATA GAG AGG ATC AGA AGA ATT GGC TCT GGC TTG GAG CAA AAT Gln Leu Ile Glu Arg Ile Arg Arg Ile Gly Ser Gly Leu Glu Gln Asn 110 115 120 125	985
5	AAC ACG ATG AAG GGA AAA GCA CCT CCA AAA TTG TCA GAG CAA AGT GAG Asn Thr Met Lys Gly Lys Ala Pro Pro Lys Leu Ser Glu Gln Ser Glu 130 135 140	1033
	AAA AAT CGA GTT CCC AGA GCT GCT ACC TCA AGA ACG GAA AGG ATA TGG Lys Asn Arg Val Pro Arg Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp 145 150 155	1081
10	CCT GGG GGT GTC ATT CCT TAT GTC ATA GGA GGA AAC TTT ACT GGC AGC Pro Gly Gly Val Ile Pro Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser 160 165 170	1129
15	CAG AGA GCC ATG TTC AAG CAG GCC ATG AGA CAC TGG GAA AAG CAC ACC Gln Arg Ala Met Phe Lys Gln Ala Met Arg His Trp Glu Lys His Thr 175 180 185	1177
	TGT GTG ACG TTC ACT GAG AGA AGT GAT GAA GAA AGT TAT ATT GTG TTC Cys Val Thr Phe Thr Glu Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe 190 195 200 205	1225
20	ACC TAC AGG CCT TGT GGA TGC TGC TCC TAT GTT GGT CGG CGG GGA AAT Thr Tyr Arg Pro Cys Gly Cys Ser Tyr Val Gly Arg Arg Gly Asn 210 215 220	1273
	GGC CCT CAG GCC ATC TCT ATT GGC AAG AAC TGT GAC AAG TTT GGA ATT Gly Pro Gln Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile 225 230 235	1321
25	GTT GTT CAT GAA CTG GGC CAC GTG ATA GGC TTC TGG CAT GAA CAT ACC Val Val His Glu Leu Gly His Val Ile Gly Phe Trp His Glu His Thr 240 245 250	1369
30	CGC CCA GAC CGA GAC AAC CAT GTC ACC ATC ATT AGA GAG AAC ATC CAG Arg Pro Asp Arg Asp Asn His Val Thr Ile Ile Arg Glu Asn Ile Gln 255 260 265	1417
	CCA GGT CAA GAG TAC AAT TTT CTA AAG ATG GAG CCT GGA GAA GTG AAC Pro Gly Gln Glu Tyr Asn Phe Leu Lys Met Glu Pro Gly Glu Val Asn 270 275 280 285	1465
35	TCT CTT GGG GAA AGA TAT GAT TTT GAC AGT ATC ATG CAC TAC GCC AGG Ser Leu Gly Glu Arg Tyr Asp Phe Asp Ser Ile Met His Tyr Ala Arg 290 295 300	1513
	AAC ACC TTC TCA AGA GGG ATG TTT TTA GAC ACA ATA CTC CCC TCC CGT Asn Thr Phe Ser Arg Gly Met Phe Leu Asp Thr Ile Leu Pro Ser Arg 305 310 315	1561
40	GAT GAT AAT GGC ATT CGT CCT GCA ATT GGT CAA CGG ACC CGG TTA AGC Asp Asp Asn Gly Ile Arg Pro Ala Ile Gly Gln Arg Thr Arg Leu Ser 320 325 330	1609
45	AAA GGA GAC ATT GCA CAA GCA AGA AAG CTG TAT CGA TGC CCA GCA TGT Lys Gly Asp Ile Ala Gln Ala Arg Lys Leu Tyr Arg Cys Pro Ala Cys 335 340 345	1657
	GGA GAA ACC CTG CAA GAA TCC AGT GGC AAC CTT TCT TCC CCA GGA TTC Gly Glu Thr Leu Gln Glu Ser Ser Gly Asn Leu Ser Ser Pro Gly Phe 350 355 360 365	1705
50	CCA AAT GGC TAC CCT TCC TAC ACA CAC TGC ATC TGG AGA GTG TCT GTG Pro Asn Gly Tyr Pro Ser Tyr Thr His Cys Ile Trp Arg Val Ser Val 370 375 380	1753

	ACC CCG GGA GAA AAG ATT GTC TTG AAT TTT ACC ACA ATG GAC CTT TAC Thr Pro Gly Glu Lys Ile Val Leu Asn Phe Thr Thr Met Asp Leu Tyr 385 390 395	1801
5	AAA AGT AGT TTG TGC TGG TAT GAT TAC ATT GAA GTA AGA GAT GGT TAC Lys Ser Ser Leu Cys Trp Tyr Asp Tyr Ile Glu Val Arg Asp Gly Tyr 400 405 410	1849
	TGG AGG AAG TCA CCT CTC CTT GGT AGA TTC TGT GGG GAC AAA GTG GCT Trp Arg Lys Ser Pro Leu Leu Gly Arg Phe Cys Gly Asp Lys Val Ala 415 420 425	1897
10	GGA GTT CTT ACA TCT ACG GAC AGC AGA ATG TGG ATT GAG TTT CGT AGC Gly Val Leu Thr Ser Thr Asp Ser Arg Met Trp Ile Glu Phe Arg Ser 430 435 440 445	1945
15	AGC AGT AAC TGG GTA GGA AAA GGG TTT GCA GCT GTC TAT GAA GCG ATT Ser Ser Asn Trp Val Gly Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile 450 455 460	1993
20	TGT GGA GGG GAG ATA AGG AAA AAC GAA GGG CAG ATT CAG TCT CCC AAT Cys Gly Gly Glu Ile Arg Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn 465 470 475	2041
25	TAC CCC GAT GAC TAC CGA CCA ATG AAG GAG TGT GTA TGG AAA ATA ATG Tyr Pro Asp Asp Tyr Arg Pro Met Lys Glu Cys Val Trp Lys Ile Met 480 485 490	2089
30	GTG TCC GAG GGC TAC CAT GTT GGA CTG ACC TTT CAG GCC TTT GAG ATC Val Ser Glu Gly Tyr His Val Gly Leu Thr Phe Gln Ala Phe Glu Ile 495 500 505	2137
35	GAA AGA CAT GAC AGC TGT GCC TAT GAC CAC CTA GAA GTT CGA GAT GGA Glu Arg His Asp Ser Cys Ala Tyr Asp His Leu Glu Val Arg Asp Gly 510 515 520 525	2185
40	GCC AGT GAG AAC AGC CCT TTG ATA GGA CGG TTC TGT GGT TAT GAC AAA Ala Ser Glu Asn Ser Pro Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys 530 535 540	2233
45	CCT GAA GAT ATA AGG TCT ACT TCC AAC ACC CTG TGG ATG AAG TTT GTC Pro Glu Asp Ile Arg Ser Thr Ser Asn Thr Leu Trp Met Lys Phe Val 545 550 555	2281
50	TCT GAC GGG ACT GTG AAC AAG GCA GGG TTT GCT GCG AAC TTT TTT AAA Ser Asp Gly Thr Val Asn Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys 560 565 570	2329
	GAG GAA GAT GAG TGT GCC AAA CCT GAC CGA GGA GGC TGT GAA CAG AGG Glu Glu Asp Glu Cys Ala Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg 575 580 585	2377
	TGT CTT AAC ACA CTA GGC AGC TAC CAG TGT GCC TGT GAG CCT GGC TAT Cys Leu Asn Thr Leu Gly Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr 590 595 600 605	2425
	GAA CTG GGG CCA GAC AGA AGC AGC TGT GAA GCT GCT TGC GGA GGA CTT Glu Leu Gly Pro Asp Arg Arg Ser Cys Glu Ala Ala Cys Gly Gly Leu 610 615 620	2473
	CTG ACG AAG CTC AAT GGC ACC ATA ACC ACC CCC GGC TGG CCC AAA GAG Leu Thr Lys Leu Asn Gly Thr Ile Thr Thr Pro Gly Trp Pro Lys Glu 625 630 635	2521
	TAC CCT CCA AAC AAA AAC TGT GTG TGG CAA GTG ATC GCG CCA AGC CAG Tyr Pro Pro Asn Lys Asn Cys Val Trp Gln Val Ile Ala Pro Ser Gln 640 645 650	2569

	TAC AGA ATC TCT GTG AAG TTT GAG TTT TTT GAA TTG GAA GGC AAT GAA Tyr Arg Ile Ser Val Lys Phe Glu Phe Glu Leu Glu Gly Asn Glu 655 660 665	2617
5	GTT TGC AAA TAC GAT TAC GTG GAG ATC TGG AGC GGC CCT TCC TCT GAG Val Cys Lys Tyr Asp Tyr Val Glu Ile Trp Ser Gly Pro Ser Ser Glu 670 675 680 685	2665
	TCT AAA CTG CAT GGC AAG TTC TGT GGC GCT GAC ATA CCT GAA GTG ATG Ser Lys Leu His Gly Lys Phe Cys Gly Ala Asp Ile Pro Glu Val Met 690 695 700	2713
10	ACT TCC CAT TTC AAC AAC ATG AGG ATT GAA TTC AAG TCA GAC AAC ACT Thr Ser His Phe Asn Asn Met Arg Ile Glu Phe Lys Ser Asp Asn Thr 705 710 715	2761
15	GTA TCC AAG AAG GGC TTC AAA GCA CAT TTT TTC TCA GAT AAG GAT GAG Val Ser Lys Lys Gly Phe Lys Ala His Phe Phe Ser Asp Lys Asp Glu 720 725 730	2809
	TGT TCA AAG GAT AAT GGT GGC TGT CAG CAT GAG TGT GTC AAC ACG ATG Cys Ser Lys Asp Asn Gly Gly Cys Gln His Glu Cys Val Asn Thr Met 735 740 745	2857
20	GGA AGT TAC ACG TGT CAG TGC CGG AAT GGA TTC GTG TTG CAT GAG AAC Gly Ser Tyr Thr Cys Gln Cys Arg Asn Gly Phe Val Leu His Glu Asn 750 755 760 765	2905
	AAG CAT GAT TGC AAG GAA GCC GAG TGT GAA CAG AAG ATA CAC AGC CCA Lys His Asp Cys Lys Glu Ala Glu Cys Glu Gln Lys Ile His Ser Pro 770 775 780	2953
25	AGT GGT CTC ATC ACC AGT CCC AAC TGG CCA GAC AAG TAT CCA AGC AGG Ser Gly Leu Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg 785 790 795	3001
30	AAA GAG TGC ACG TGG GTG ATC AGT GCC ATT CCT GGC CAC CGC ATC ACA Lys Glu Cys Thr Trp Val Ile Ser Ala Ile Pro Gly His Arg Ile Thr 800 805 810	3049
	TTA GCC TTC AAT GAG TTT GAG GTT GAA CAA CAT CAA GAA TGT GCT TAT Leu Ala Phe Asn Glu Phe Glu Val Glu Gln His Gln Glu Cys Ala Tyr 815 820 825	3097
35	GAT CAC TTG GAA ATT TTT GAT GGA GAA ACG GAG AAG TCA CCA ATA CTT Asp His Leu Glu Ile Phe Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu 830 835 840 845	3145
	GGC CGA CTA TGT GGC AGC AAG ATA CCA GAT CCC CTC ATG GCT ACT GGG Gly Arg Leu Cys Gly Ser Lys Ile Pro Asp Pro Leu Met Ala Thr Gly 850 855 860	3193
40	AAT GAA ATG TTT ATT CGG TTT ATT TCT GAT GCC TCT GTT CAA AGA AAA Asn Glu Met Phe Ile Arg Phe Ile Ser Asp Ala Ser Val Gln Arg Lys 865 870 875	3241
	GGC TTT CAA GCT ACA CAT TCC ACA GAG TGT GGT CGA TTG AAA GCA Gly Phe Gln Ala Thr His Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala 880 885 890	3289
45	GAG TCA AAG CCT AGA GAC CTG TAC TCC CAT GCT CAG TTT GGT GAT AAT Glu Ser Lys Pro Arg Asp Leu Tyr Ser His Ala Gln Phe Gly Asp Asn 895 900 905	3337
50	AAC TAC CCA GGA CAA CTG GAC TGT GAA TGG TTG TTG GTG TCA GAA CGA Asn Tyr Pro Gly Gln Leu Asp Cys Glu Trp Leu Leu Val Ser Glu Arg 910 915 920 925	3385

TOP SECRET - 999999

	GGA TCT CGA CTT GAA TTG TCC TTC CAG ACA TTC GAA GTC GAA GAA GAA	3433
	Gly Ser Arg Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Glu	
	930 935 940	
5	GCT GAC TGT GGC TAT GAC TAT GTT GAA GTC TTT GAT GGT CTC AGT TCA	3481
	Ala Asp Cys Gly Tyr Asp Tyr Val Glu Val Phe Asp Gly Leu Ser Ser	
	945 950 955	
	AAA GCT GTG GGT CTT GGT AGA TTC TGT GGG TCA GGG CCA CCA GAA GAA	3529
	Lys Ala Val Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu	
	960 965 970	
10	ATC TAT TCA ATT GGA GAT GTG GCT TTG ATT CAT TTC CAC ACA GAT GAC	3577
	Ile Tyr Ser Ile Gly Asp Val Ala Leu Ile His Phe His Thr Asp Asp	
	975 980 985	
15	ACT ATC AAC AAG AAA GGA TTT TAT ATA AGA TAT AAA AGT ATA AGA TAC	3625
	Thr Ile Asn Lys Lys Gly Phe Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr	
	990 995 1000 1005	
	CCG GAA ACG ATG CAT GCC AAG AAC TAA TGCCGACCCCT CCCTCAGAAC	3672
	Pro Glu Thr Met His Ala Lys Asn *	
	1010	
	AGAAAGGAAT GTGCATATGG AAAGAAGACA TTTTTAAAAT AGACAATATT AATACAATTG	3732
20	TTTTATATAA TGAATTTGAG CAAAAGAAC CTGCAAGATT AGAGTTATCT CTGAAGTGAA	3792
	AGAGAACTTT CCAGAAAACC TGATTGGCAT TGCAAGGATG TTTGAAAGTC ATGCTTGTTC	3852
	AAGGAAGATT AACAGCTTGA AATAGATGCT TCACATTTG GACAGTCAT TTAATGAGCT	3912
	GTGATTCTCT GGAGTGATTT CTTGACTACT TTTCCAAGAT CTGGGGACGT AGAAATGATG	3972
	GGACGGATCA TAGCTTGAA ACCCACTTCT TGGGTCTTAG CATGTTGCT TAGACTCTGT	4032
25	AGGTCAAGACA CAGTGTAAAC CAAATTCAATG TAAGGTGATG TGGAATAGTG GTCTTTGGAA	4092
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	TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGCGTG TGTGTGTGTG TGCGTGTGTG	4212
	TGTGTGTGCA TGTGTGTGCA TGTGTGTTG GAAACTGGAA TATTCATCT TCATTATTTT	4272
	CAAATGCAGG CCAGCTTAAC CTGTTCACAC AAATGATTT GTGACCACCT CATTGTATCT	4332
30	GTATCTTGAG AAGTTTGAAA TATCTATAGT GTCTACAATG CAGTTAATCC CTAGATATCG	4392
	GATAATAACCC AGTTCACTAG TAAACTCATT TCTCTCTGGG GAAGTGCTGA ATAGTCTCCA	4452
	AATTCAAGAA ACTCACCATG TCTTATAAAC CTTTAAGATA AAATTCCAAC GAGGTGTGTG	4512
	CAGCCATCTT CCAAATGACT GCCTGGATGT TTCTTAGTCC AGTTACTACT GCTGCTGCTA	4572
	TTGGTCTTTC TTTTATTGTT AATGTGTGTA TATGTTGTTA TTATTATGGT TATTATTATT	4632
35	GATGTTGTTA CTATATTAA AAATGATGAG ATGAAGTGGG AGTAGAGTTT GGGAGAAATG	4692
	AAATCTCTCT TTTTTGTTCT CTTCTTGAAA TTCAGTTCA AAAAATACAA TATTGGGTGG	4752
	CAAAAAAAA AAAAAAAA	4771

5 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1014 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp Leu Val Val
1 5 10 15

10 Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala Gly Leu Asp
20 25 30

Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Pro Ile
35 40 45

Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala
50 55 60

Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg Thr Ile Asp
65 70 75 80

Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr Gly Gly Phe
85 90 95

Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr Gln Leu Ile
100 105 110

Glu Arg Ile Arg Arg Ile Gly Ser Gly Leu Glu Gln Asn Asn Thr Met
115 120 125

Lys Gly Lys Ala Pro Pro Lys Leu Ser Glu Gln Ser Glu Lys Asn Arg
130 135 140

Val Pro Arg Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp Pro Gly Gly
145 150 155 160

Val Ile Pro Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln Arg Ala
165 170 175

30 Met Phe Lys Gln Ala Met Arg His Trp Glu Lys His Thr Cys Val Thr
180 185 190

Phe Thr Glu Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe Thr Tyr Arg
195 200 205

Pro Cys Gly Cys Cys Ser Tyr Val Gly Arg Arg Gly Asn Gly Pro Gln
210 215 220

Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile Val Val His
225 230 235 240

Glu Leu Gly His Val Ile Gly Phe Trp His Glu His Thr Arg Pro Asp
245 250 255

40 Arg Asp Asn His Val Thr Ile Ile Arg Glu Asn Ile Gln Pro Gly Gln
260 265 270

Glu Tyr Asn Phe Leu Lys Met Glu Pro Gly Glu Val Asn Ser Leu Gly
275 280 285

Glu Arg Tyr Asp Phe Asp Ser Ile Met His Tyr Ala Arg Asn Thr Phe
45 290 295 300

Ser Arg Gly Met Phe Leu Asp Thr Ile Leu Pro Ser Arg Asp Asp Asn
 305 310 315 320
 Gly Ile Arg Pro Ala Ile Gly Gln Arg Thr Arg Leu Ser Lys Gly Asp
 325 330 335
 5 Ile Ala Gln Ala Arg Lys Leu Tyr Arg Cys Pro Ala Cys Gly Glu Thr
 340 345 350
 Leu Gln Glu Ser Ser Gly Asn Leu Ser Ser Pro Gly Phe Pro Asn Gly
 355 360 365
 Tyr Pro Ser Tyr Thr His Cys Ile Trp Arg Val Ser Val Thr Pro Gly
 10 370 375 380
 Glu Lys Ile Val Leu Asn Phe Thr Thr Met Asp Leu Tyr Lys Ser Ser
 385 390 395 400
 Leu Cys Trp Tyr Asp Tyr Ile Glu Val Arg Asp Gly Tyr Trp Arg Lys
 405 410 415
 15 Ser Pro Leu Leu Gly Arg Phe Cys Gly Asp Lys Val Ala Gly Val Leu
 420 425 430
 Thr Ser Thr Asp Ser Arg Met Trp Ile Glu Phe Arg Ser Ser Ser Asn
 435 440 445
 20 Trp Val Gly Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile Cys Gly Gly
 450 455 460
 Glu Ile Arg Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn Tyr Pro Asp
 465 470 475 480
 Asp Tyr Arg Pro Met Lys Glu Cys Val Trp Lys Ile Met Val Ser Glu
 485 490 495
 25 Gly Tyr His Val Gly Leu Thr Phe Gln Ala Phe Glu Ile Glu Arg His
 500 505 510
 Asp Ser Cys Ala Tyr Asp His Leu Glu Val Arg Asp Gly Ala Ser Glu
 515 520 525
 30 Asn Ser Pro Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys Pro Glu Asp
 530 535 540
 Ile Arg Ser Thr Ser Asn Thr Leu Trp Met Lys Phe Val Ser Asp Gly
 545 550 555 560
 Thr Val Asn Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys Glu Glu Asp
 565 570 575
 35 Glu Cys Ala Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg Cys Leu Asn
 580 585 590
 Thr Leu Gly Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr Glu Leu Gly
 595 600 605
 40 Pro Asp Arg Arg Ser Cys Glu Ala Ala Cys Gly Gly Leu Leu Thr Lys
 610 615 620
 Leu Asn Gly Thr Ile Thr Thr Pro Gly Trp Pro Lys Glu Tyr Pro Pro
 625 630 635 640
 Asn Lys Asn Cys Val Trp Gln Val Ile Ala Pro Ser Gln Tyr Arg Ile
 645 650 655

Ser Val Lys Phe Glu Phe Glu Leu Glu Gly Asn Glu Val Cys Lys
 660 665 670
 Tyr Asp Tyr Val Glu Ile Trp Ser Gly Pro Ser Ser Glu Ser Lys Leu
 675 680 685
 5 His Gly Lys Phe Cys Gly Ala Asp Ile Pro Glu Val Met Thr Ser His
 690 695 700
 Phe Asn Asn Met Arg Ile Glu Phe Lys Ser Asp Asn Thr Val Ser Lys
 705 710 715 720
 10 Lys Gly Phe Lys Ala His Phe Phe Ser Asp Lys Asp Glu Cys Ser Lys
 725 730 735
 Asp Asn Gly Gly Cys Gln His Glu Cys Val Asn Thr Met Gly Ser Tyr
 740 745 750
 Thr Cys Gln Cys Arg Asn Gly Phe Val Leu His Glu Asn Lys His Asp
 755 760 765
 15 Cys Lys Glu Ala Glu Cys Glu Gln Lys Ile His Ser Pro Ser Gly Leu
 770 775 780
 Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg Lys Glu Cys
 785 790 795 800
 20 Thr Trp Val Ile Ser Ala Ile Pro Gly His Arg Ile Thr Leu Ala Phe
 805 810 815
 Asn Glu Phe Glu Val Glu Gln His Gln Glu Cys Ala Tyr Asp His Leu
 820 825 830
 Glu Ile Phe Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu Gly Arg Leu
 835 840 845
 25 Cys Gly Ser Lys Ile Pro Asp Pro Leu Met Ala Thr Gly Asn Glu Met
 850 855 860
 Phe Ile Arg Phe Ile Ser Asp Ala Ser Val Gln Arg Lys Gly Phe Gln
 865 870 875 880
 30 Ala Thr His Ser Thr Glu Cys Gly Arg Leu Lys Ala Glu Ser Lys
 885 890 895
 Pro Arg Asp Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro
 900 905 910
 Gly Gln Leu Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg
 915 920 925
 35 Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Ala Asp Cys
 930 935 940
 Gly Tyr Asp Tyr Val Glu Val Phe Asp Gly Leu Ser Ser Lys Ala Val
 945 950 955 960
 40 Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser
 965 970 975
 Ile Gly Asp Val Ala Leu Ile His Phe His Thr Asp Asp Thr Ile Asn
 980 985 990
 Lys Lys Gly Phe Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Glu Thr
 995 1000 1005

Met His Ala Lys Asn *
1010

(2) INFORMATION FOR SEQ ID NO:4:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

20 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 648..3689
25 (D) OTHER INFORMATION: /product= "human mT11 protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTCACACTTT TGCTCTCTTG CAGTCAGTTG CTTTGCTGGC TTCTGCAGGC TTTTAAGGTC 60
TCGGCGCGTA GAAATGCCTG GCCCCCACCC CCTTCCTCGG TCTCCCTTT CAATTCAAGAT 120
GTGCTGATGT GCAGACCGGA TTCATCTTCT CGGAGCTGCG GCGGCGGCTT TGGGCTCAGG 180
CGGCGGCGGC TCGCGCTCGG CCGCGGAGTC CTGGCAGCAG CGGGGACGCG GCGCGGGAGT 240
CCGAGCTCTG GTGGCAGCTG AGCCCGCGGG GCGCCGCTCG CCGAGCCGCG GCGCGGGAA 300
GTTCCGGCAGC CAGAAGGACG ACCTGGCAGG CTGCGAGCGC CAGCGCCGCC AGAGCCGAGT 360
TTGCCTGCGC CCTCCCCGCC TCCGAGTGCA GAGTTCCCTTA CCTGCCCTCC GCCCACCCGT 420
GGGCCCCTAG CCAACTTCTC CCTGCGACTG GGGGTAACAG GCAGTGCTTG CCCTCTCTAC 480
25 TGTCCCGGCG GCATCCACAT GTTCCGGAC ACCTGAGCAC CCCGGTCCCC CCGAGGAGCC 540
TCCGGGTGGG GAGAAGAGCA CCGGTGCCCC TAGCCCCGCA CATCAGCGCG GACCGCCGCT 600
GCCTAACCTC TGGGTCCCGT CCCCTCCTTT TCCTCCGGGG GAGGAGG ATG GGG TTG 656
Met Gly Leu
1015

30 GGA ACG CTT TCC CCG AGG ATG CTC GTG TGG CTG GTG GCC TCG GGG ATT 704
Gly Thr Leu Ser Pro Arg Met Leu Val Trp Leu Val Ala Ser Gly Ile
1020 1025 1030

35 GTT TTC TAC GGG GAG CTA TGG GTC TGC GCT GGC CTC GAT TAT GAT TAC 752
Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly Leu Asp Tyr Asp Tyr
1035 1040 1045

ACT TTT GAT GGG AAC GAA GAG GAT AAA ACA GAG ACT ATA GAT TAC AAG 800
Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Thr Ile Asp Tyr Lys
1050 1055 1060 1065

40 GAC CCG TGT AAA GCC GCT GTA TTT TGG GGC GAT ATT GCC TTA GAT GAT 848
Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala Leu Asp Asp
1070 1075 1080

GAA GAC TTA AAT ATC TTT CAA ATA GAT AGG ACA ATT GAC CTT ACG CAG 896
 Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg Thr Ile Asp Leu Thr Gln
 1085 1090 1095

5 AAC CCC TTT GGA AAC CTT GGA CAT ACC ACA GGT GGA CTT GGA GAC CAT 944
 Asn Pro Phe Gly Asn Leu Gly His Thr Thr Gly Gly Leu Gly Asp His
 1100 1105 1110

GCT ATG TCA AAG AAG CGA GGG GCC CTC TAC CAA CTT ATA GAC AGG ATA 992
 Ala Met Ser Lys Lys Arg Gly Ala Leu Tyr Gln Leu Ile Asp Arg Ile
 1115 1120 1125

10 AGA AGA ATT GGC TTT GGC TTG GAG CAA AAC AAC ACA GTT AAG GGA AAA 1040
 Arg Arg Ile Gly Phe Gly Leu Glu Gln Asn Asn Thr Val Lys Gly Lys
 1130 1135 1140 1145

15 GTA CCT CTA CAA TTC TCA GGG CAA AAT GAG AAA AAT CGA GTT CCC AGA 1088
 Val Pro Leu Gln Phe Ser Gly Gln Asn Glu Lys Asn Arg Val Pro Arg
 1150 1155 1160

GCC GCT ACA TCA AGA ACG GAA AGA ATA TGG CCT GGA GGC GTT ATT CCT 1136
 Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp Pro Gly Gly Val Ile Pro
 1165 1170 1175

20 TAT GTT ATA GGA GGA AAC TTC ACT GGC AGC CAG AGA GCC ATG TTC AAG 1184
 Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln Arg Ala Met Phe Lys
 1180 1185 1190

CAG GCC ATG AGG CAC TGG GAA AAG CAC ACA TGT GTG ACT TTC ATA GAA 1232
 Gln Ala Met Arg His Trp Glu Lys His Thr Cys Val Thr Phe Ile Glu
 1195 1200 1205

25 AGA AGT GAT GAA GAG AGT TAC ATT GTA TTC ACC TAT AGG CCT TGT GGA 1280
 Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe Thr Tyr Arg Pro Cys Gly
 1210 1215 1220 1225

TGC TGC TCC TAT GTA GGT CGG CGA GGA AAT GGA CCT CAG GCA ATC TCT 1328
 Cys Cys Ser Tyr Val Gly Arg Arg Gly Asn Gly Pro Gln Ala Ile Ser
 1230 1235 1240

ATC GGC AAG AAC TGT GAT AAA TTT GGG ATT GTT GTT CAT GAA TTG GGT 1376
 Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile Val Val His Glu Leu Gly
 1245 1250 1255

35 CAT GTG ATA GGC TTT TGG CAT GAA CAC ACA AGA CCA GAT CGA GAT AAC 1424
 His Val Ile Gly Phe Trp His Glu His Thr Arg Pro Asp Arg Asp Asn
 1260 1265 1270

CAC GTA ACT ATC ATA AGA GAA AAC ATC CAG CCA GGT CAA GAG TAC AAT 1472
 His Val Thr Ile Ile Arg Glu Asn Ile Gln Pro Gly Gln Glu Tyr Asn
 1275 1280 1285

40 TTT CTG AAG ATG GAG CCT GGA GAA GTA AAC TCA CTT GGA GAA AGA TAT 1520
 Phe Leu Lys Met Glu Pro Gly Glu Val Asn Ser Leu Gly Glu Arg Tyr
 1290 1295 1300 1305

45 GAT TTC GAC AGT ATC ATG CAC TAT GCC AGG AAC ACC TTC TCA AGG GGG 1568
 Asp Phe Asp Ser Ile Met His Tyr Ala Arg Asn Thr Phe Ser Arg Gly
 1310 1315 1320

ATG TTT CTG GAT ACC ATT CTC CCC TCC CGT GAT GAT AAT GGC ATA CGT 1616
 Met Phe Leu Asp Thr Ile Leu Pro Ser Arg Asp Asp Asn Gly Ile Arg
 1325 1330 1335

50 CCT GCA ATT GGT CAG CGA ACC CGT CTA AGC AAA GGA GAT ATC GCA CAG 1664
 Pro Ala Ile Gly Gln Arg Thr Arg Leu Ser Lys Gly Asp Ile Ala Gln
 1340 1345 1350

	GCA AGA AAG CTG TAT AGA TGT CCA GCA TGT GGA GAA ACT CTA CAA GAA Ala Arg Lys Leu Tyr Arg Cys Pro Ala Cys Gly Glu Thr Leu Gln Glu 1355 1360 1365	1712
5	TCC AAT GGC AAC CTT TCC TCT CCA GGA TTT CCC AAT GGC TAC CCT TCT Ser Asn Gly Asn Leu Ser Ser Pro Gly Phe Pro Asn Gly Tyr Pro Ser 1370 1375 1380 1385	1760
	TAC ACA CAC TGC ATC TGG AGA GTT TCT GTG ACC CCA GGG GAG AAG ATT Tyr Thr His Cys Ile Trp Arg Val Ser Val Thr Pro Gly Glu Lys Ile 1390 1395 1400	1808
10	GTT TTA AAT TTT ACA ACG ATG GAT CTA TAC AAG AGT AGT TTG TGC TGG Val Leu Asn Phe Thr Thr Met Asp Leu Tyr Lys Ser Ser Leu Cys Trp 1405 1410 1415	1856
15	TAT GAC TAT ATT GAA GTA AGA GAC GGG TAC TGG AGA AAA TCA CCT CTC Tyr Asp Tyr Ile Glu Val Arg Asp Gly Tyr Trp Arg Lys Ser Pro Leu 1420 1425 1430	1904
20	□ CTT GGT AGA TTC TGT GGG GAC AAA TTG CCT GAA GTT CTT ACT TCT ACA Leu Gly Arg Phe Cys Gly Asp Lys Leu Pro Glu Val Leu Thr Ser Thr 1435 1440 1445	1952
	GAC AGC AGA ATG TGG ATT GAG TTT CGT AGC AGC AGT AAT TGG GTA GGA Asp Ser Arg Met Trp Ile Glu Phe Arg Ser Ser Ser Asn Trp Val Gly 1450 1455 1460 1465	2000
	AAA GGC TTT GCA GCT GTC TAT GAA GCG ATC TGT GGA GGT GAG ATA CGT Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile Cys Gly Gly Glu Ile Arg 1470 1475 1480	2048
25	AAA AAT GAA GGA CAG ATT CAG TCT CCC AAT TAT CCT GAT GAC TAT CGC Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn Tyr Pro Asp Asp Tyr Arg 1485 1490 1495	2096
30	CCG ATG AAA GAA TGT GTG TGG AAA ATA ACA GTG TCT GAG AGC TAC CAC Pro Met Lys Glu Cys Val Trp Lys Ile Thr Val Ser Glu Ser Tyr His 1500 1505 1510	2144
	GTC GGG CTG ACC TTT CAG TCC TTT GAG ATT GAA AGA CAT GAC AAT TGT Val Gly Leu Thr Phe Gln Ser Phe Glu Ile Glu Arg His Asp Asn Cys 1515 1520 1525	2192
35	GCT TAT GAC TAC CTG GAA GTT AGA GAT GGA ACC AGT GAA AAT AGC CCT Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly Thr Ser Glu Asn Ser Pro 1530 1535 1540 1545	2240
	TTG ATA GGG CGT TTC TGT GGT TAT GAC AAA CCT GAA GAC ATA AGA TCT Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys Pro Glu Asp Ile Arg Ser 1550 1555 1560	2288
40	ACC TCC AAT ACT TTG TGG ATG AAG TTT GTT TCT GAC GGA ACT GTG AAC Thr Ser Asn Thr Leu Trp Met Lys Phe Val Ser Asp Gly Thr Val Asn 1565 1570 1575	2336
45	AAA GCA GGG TTT GCT GCT AAC TTT AAA GAG GAA GAT GAG TGT GCC Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys Glu Glu Asp Glu Cys Ala 1580 1585 1590	2384
	AAA CCT GAC CGT GGA GGC TGT GAG CAG CGA TGT CTG AAC ACT CTG GGC Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg Cys Leu Asn Thr Leu Gly 1595 1600 1605	2432
50	AGT TAC CAG TGT GCC TGT GAG CCT GGC TAT GAG CTG GGC CCA GAC AGA Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr Glu Leu Gly Pro Asp Arg 1610 1615 1620 1625	2480

	AGG AGC TGT GAA GCT GCT TGT GGT GGA CTT CTT ACC AAA CTT AAC GGC	2528
	Arg Ser Cys Glu Ala Ala Cys Gly Gly Leu Leu Thr Lys Leu Asn Gly	
	1630 1635 1640	
5	ACC ATA ACC ACC CCT GGC TGG CCC AAG GAG TAC CCT CCT AAT AAG AAC	2576
	Thr Ile Thr Thr Pro Gly Trp Pro Lys Glu Tyr Pro Pro Asn Lys Asn	
	1645 1650 1655	
	TGT GTG TGG CAA GTG GTT GCA CCA ACC CAG TAC AGA ATT TCT GTG AAG	2624
	Cys Val Trp Gln Val Val Ala Pro Thr Gln Tyr Arg Ile Ser Val Lys	
	1660 1665 1670	
10	TTT GAG TTT TTT GAA TTG GAA GGC AAT GAA GTT TGC AAA TAT GAT TAT	2672
	Phe Glu Phe Phe Glu Leu Glu Gly Asn Glu Val Cys Lys Tyr Asp Tyr	
	1675 1680 1685	
15	GTG GAG ATC TGG AGT GGT CTT TCC TCT GAG TCT AAA CTG CAT GGC AAA	2720
	Val Glu Ile Trp Ser Gly Leu Ser Ser Glu Ser Lys Leu His Gly Lys	
	1690 1695 1700 1705	
20	TTC TGT GGC GCT GAA GTG CCT GAA GTG ATC ACA TCC CAG TTC AAC AAT	2768
	Phe Cys Gly Ala Glu Val Pro Glu Val Ile Thr Ser Gln Phe Asn Asn	
	1710 1715 1720	
25	ATG AGA ATT GAA TTC AAA TCT GAC AAT ACT GTA TCC AAG AAG GGC TTC	2816
	Met Arg Ile Glu Phe Lys Ser Asp Asn Thr Val Ser Lys Lys Gly Phe	
	1725 1730 1735	
30	AAA GCA CAT TTT TTC TCA GAC AAA GAT GAA TGC TCT AAG GAT AAT GGT	2864
	Lys Ala His Phe Phe Ser Asp Lys Asp Glu Cys Ser Lys Asp Asn Gly	
	1740 1745 1750	
35	GGA TGT CAG CAC GAA TGT GTC AAC ACG ATG GGG AGC TAC ATG TGT CAA	2912
	Gly Cys Gln His Glu Cys Val Asn Thr Met Gly Ser Tyr Met Cys Gln	
	1755 1760 1765	
40	TGC CGT AAT GGA TTT GTG CTA CAT GAC AAT AAA CAT GAT TGC AAG GAA	2960
	Cys Arg Asn Gly Phe Val Leu His Asp Asn Lys His Asp Cys Lys Glu	
	1770 1775 1780 1785	
45	GCT GAG TGT GAA CAG AAG ATC CAC AGT CCA AGT GGC CTC ATC ACC AGT	3008
	Ala Glu Cys Glu Gln Lys Ile His Ser Pro Ser Gly Leu Ile Thr Ser	
	1790 1795 1800	
50	CCC AAC TGG CCA GAC AAG TAC CCA AGC AGG AAA GAA TGC ACT TGG GAA	3056
	Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg Lys Glu Cys Thr Trp Glu	
	1805 1810 1815	
	ATC AGC GCC ACT CCC GGC CAC CGA ATC AAA TTA GCC TTT AGT GAA TTT	3104
	Ile Ser Ala Thr Pro Gly His Arg Ile Lys Leu Ala Phe Ser Glu Phe	
	1820 1825 1830	
55	GAG ATT GAG CAG CAT CAA GAA TGT GCT TAT GAC CAC TTA GAA GTA TTT	3152
	Glu Ile Glu Gln His Gln Glu Cys Ala Tyr Asp His Leu Glu Val Phe	
	1835 1840 1845	
60	GAT GGA GAA ACA GAA AAG TCA CCG ATT CTT GGA CGA CTA TGT GGC AAC	3200
	Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu Gly Arg Leu Cys Gly Asn	
	1850 1855 1860 1865	
65	AAG ATA CCA GAT CCC CTT GTG GCT ACT GGA AAT AAA ATG TTT GTT CGG	3248
	Lys Ile Pro Asp Pro Leu Val Ala Thr Gly Asn Lys Met Phe Val Arg	
	1870 1875 1880	
70	TTT GTT TCT GAT GCA TCT GTT CAA AGA AAA GGC TTT CAA GCC ACA CAT	3296
	Phe Val Ser Asp Ala Ser Val Gln Arg Lys Gly Phe Gln Ala Thr His	
	1885 1890 1895	

TCT ACA GAG TGT GGC GGA CGA TTG AAA GCA GAA TCA AAA CCA AGA GAT 3344
 Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala Glu Ser Lys Pro Arg Asp
 1900 1905 1910
 CTG TAC TCA CAT GCT CAG TTT GGT GAT AAC AAC TAC CCA GGA CAG GTT 3392
 5 Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro Gly Gln Val
 1915 1920 1925
 GAC TGT GAA TGG CTA TTA GTA TCA GAA CGG GGC TCT CGA CTT GAA TTA 3440
 Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg Leu Glu Leu
 1930 1935 1940 1945
 10 TCC TTC CAG ACA TTT GAA GTG GAG GAA GCA GAC TGT GGC TAT GAC 3488
 Ser Phe Gln Thr Phe Glu Val Glu Glu Ala Asp Cys Gly Tyr Asp
 1950 1955 1960
 TAT GTG GAG CTC TTT GAT GGT CTT GAT TCA ACA GCT GTG GGG CTT GGT 3536
 15 Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val Gly Leu Gly
 1965 1970 1975
 CGA TTC TGT GGA TCC GGG CCA CCA GAA GAG ATT TAT TCA ATT GGA GAT 3584
 Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser Ile Gly Asp
 1980 1985 1990
 TCA GTT TTA ATT CAT TTC CAC ACT GAT GAC ACA ATC AAC AAG AAG GGA 3632
 Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn Lys Lys Gly
 1995 2000 2005
 TTT CAT ATA AGA TAC AAA AGC ATA AGA TAT CCA GAT ACC ACA CAT ACC 3680
 Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr
 2010 2015 2020 2025
 AAA AAA TAA CACCAAAACC TCTGTCAGAA CACAAAGGAA TGTGCATAAT 3729
 Lys Lys *
 GGAGAGAAGA CATATTTTT TTAAAACCTGA AGATATTGGC ACAATGTT TATACAAAGA 3789
 GTTTGAACAA AAAATCCCTG TAAGACCAGA ATTATCTTG TACTAAAAGA GAAGTTCCA 3849
 30 GCAAAACCT CATCAGCATT ACAAGGATAT TTGAACCTCCA TGCTTGATGG TATTAATAAA 3909
 GCTGGTGAAA 3919

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 1014 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

40 Met Gly Leu Gly Thr Leu Ser Pro Arg Met Leu Val Trp Leu Val Ala
 1 5 10 15

Ser Gly Ile Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly Leu Asp
 20 25 30

Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Thr Ile
 35 40 45

45 Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala
 50 55 60

Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg Thr Ile Asp
 65 70 75 80

Leu Thr Gln Asn Pro Phe Gly Asn Leu Gly His Thr Thr Gly Gly Leu
 85 90 95

5 Gly Asp His Ala Met Ser Lys Lys Arg Gly Ala Leu Tyr Gln Leu Ile
 100 105 110

Asp Arg Ile Arg Arg Ile Gly Phe Gly Leu Glu Gln Asn Asn Thr Val
 115 120 125

10 Lys Gly Lys Val Pro Leu Gln Phe Ser Gly Gln Asn Glu Lys Asn Arg
 130 135 140

Val Pro Arg Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp Pro Gly Gly
 145 150 155 160

Val Ile Pro Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln Arg Ala
 165 170 175

15 Met Phe Lys Gln Ala Met Arg His Trp Glu Lys His Thr Cys Val Thr
 180 185 190

Phe Ile Glu Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe Thr Tyr Arg
 195 200 205

20 Pro Cys Gly Cys Cys Ser Tyr Val Gly Arg Arg Gly Asn Gly Pro Gln
 210 215 220

Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile Val Val His
 225 230 235 240

Glu Leu Gly His Val Ile Gly Phe Trp His Glu His Thr Arg Pro Asp
 245 250 255

25 Arg Asp Asn His Val Thr Ile Ile Arg Glu Asn Ile Gln Pro Gly Gln
 260 265 270

Glu Tyr Asn Phe Leu Lys Met Glu Pro Gly Glu Val Asn Ser Leu Gly
 275 280 285

30 Glu Arg Tyr Asp Phe Asp Ser Ile Met His Tyr Ala Arg Asn Thr Phe
 290 295 300

Ser Arg Gly Met Phe Leu Asp Thr Ile Leu Pro Ser Arg Asp Asn
 305 310 315 320

Gly Ile Arg Pro Ala Ile Gly Gln Arg Thr Arg Leu Ser Lys Gly Asp
 325 330 335

35 Ile Ala Gln Ala Arg Lys Leu Tyr Arg Cys Pro Ala Cys Gly Glu Thr
 340 345 350

Leu Gln Glu Ser Asn Gly Asn Leu Ser Ser Pro Gly Phe Pro Asn Gly
 355 360 365

40 Tyr Pro Ser Tyr Thr His Cys Ile Trp Arg Val Ser Val Thr Pro Gly
 370 375 380

Glu Lys Ile Val Leu Asn Phe Thr Thr Met Asp Leu Tyr Lys Ser Ser
 385 390 395 400

Leu Cys Trp Tyr Asp Tyr Ile Glu Val Arg Asp Gly Tyr Trp Arg Lys
 405 410 415

Ser Pro Leu Leu Gly Arg Phe Cys Gly Asp Lys Leu Pro Glu Val Leu
 420 425 430
 Thr Ser Thr Asp Ser Arg Met Trp Ile Glu Phe Arg Ser Ser Ser Asn
 435 440 445
 5 Trp Val Gly Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile Cys Gly Gly
 450 455 460
 Glu Ile Arg Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn Tyr Pro Asp
 465 470 475 480
 10 Asp Tyr Arg Pro Met Lys Glu Cys Val Trp Lys Ile Thr Val Ser Glu
 485 490 495
 Ser Tyr His Val Gly Leu Thr Phe Gln Ser Phe Glu Ile Glu Arg His
 500 505 510
 Asp Asn Cys Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly Thr Ser Glu
 515 520 525
 15 Asn Ser Pro Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys Pro Glu Asp
 530 535 540
 Ile Arg Ser Thr Ser Asn Thr Leu Trp Met Lys Phe Val Ser Asp Gly
 545 550 555 560
 20 Thr Val Asn Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys Glu Glu Asp
 565 570 575
 Glu Cys Ala Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg Cys Leu Asn
 580 585 590
 25 Thr Leu Gly Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr Glu Leu Gly
 595 600 605
 Pro Asp Arg Arg Ser Cys Glu Ala Ala Cys Gly Gly Leu Leu Thr Lys
 610 615 620
 30 Leu Asn Gly Thr Ile Thr Pro Gly Trp Pro Lys Glu Tyr Pro Pro
 625 630 635 640
 Asn Lys Asn Cys Val Trp Gln Val Val Ala Pro Thr Gln Tyr Arg Ile
 645 650 655
 Ser Val Lys Phe Glu Phe Glu Leu Glu Gly Asn Glu Val Cys Lys
 660 665 670
 Tyr Asp Tyr Val Glu Ile Trp Ser Gly Leu Ser Ser Glu Ser Lys Leu
 675 680 685
 35 His Gly Lys Phe Cys Gly Ala Glu Val Pro Glu Val Ile Thr Ser Gln
 690 695 700
 Phe Asn Asn Met Arg Ile Glu Phe Lys Ser Asp Asn Thr Val Ser Lys
 705 710 715 720
 40 Lys Gly Phe Lys Ala His Phe Phe Ser Asp Lys Asp Glu Cys Ser Lys
 725 730 735
 Asp Asn Gly Gly Cys Gln His Glu Cys Val Asn Thr Met Gly Ser Tyr
 740 745 750
 Met Cys Gln Cys Arg Asn Gly Phe Val Leu His Asp Asn Lys His Asp
 755 760 765

Cys Lys Glu Ala Glu Cys Glu Gln Lys Ile His Ser Pro Ser Gly Leu
 770 775 780
 Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg Lys Glu Cys
 785 790 795 800
 5 Thr Trp Glu Ile Ser Ala Thr Pro Gly His Arg Ile Lys Leu Ala Phe
 805 810 815
 Ser Glu Phe Glu Ile Glu Gln His Gln Glu Cys Ala Tyr Asp His Leu
 820 825 830
 10 Glu Val Phe Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu Gly Arg Leu
 835 840 845
 Cys Gly Asn Lys Ile Pro Asp Pro Leu Val Ala Thr Gly Asn Lys Met
 850 855 860
 Phe Val Arg Phe Val Ser Asp Ala Ser Val Gln Arg Lys Gly Phe Gln
 865 870 875 880
 Ala Thr His Ser Thr Glu Cys Gly Arg Leu Lys Ala Glu Ser Lys
 885 890 895
 Pro Arg Asp Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro
 900 905 910
 Gly Gln Val Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg
 915 920 925
 Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Ala Asp Cys
 930 935 940
 Gly Tyr Asp Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val
 945 950 955 960
 Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser
 965 970 975
 Ile Gly Asp Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn
 980 985 990
 30 Lys Lys Gly Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr
 995 1000 1005
 Thr His Thr Lys Lys *
 1010

(2) INFORMATION FOR SEQ ID NO:6:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCAGCTTAAC CTGTTCACAC

20

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACTCTACTT CCACTTCATC

20

15 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGAACAGA AAGGAATGTG

20

25 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer"

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACCACTATT CCACATCACC

20

35 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTTGCAGTC AGTTGCTTG CTGG

24

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10 TAGTGCGGCC GCACATTCTT TTGTGTTTC

28

(2) INFORMATION FOR SEQ ID NO:12:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

20 Cys Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Glu Thr Met His Ala
1 5 10 15
Lys Asn

(2) INFORMATION FOR SEQ ID NO:13:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr
1 5 10 15
Lys Lys